

Fig. 1A

S	Q	A	V	A	T	K	C	Q	A	A	T	T	E	E	R	V	A	A	146	
AGC	CAG	GCC	GTG	GCC	ACC	AAG	TGC	CAA	GCA	GCC	ACC	ACT	GAG	GAA	GAG	CGA	GTG	GCT	GCA	438
V	T	L	R	K	A	E	A	M	A	F	L	Q	E	Q	P	F	K	D	F	166
GTG	ACG	CTG	CGC	AAG	GCT	GAG	GCC	ATG	GCT	TTC	TTG	CAA	GAG	CAG	CCC	TTT	AAG	GAT	TTC	498
V	T	S	A	F	Y	D	K	F	L	Q	W	K	L	F	E	M	Q	P	V	186
GTG	ACC	AGC	GCC	TTC	TAC	GAC	AAG	TTT	CTG	CAG	TGG	AAA	CTC	TTC	GAG	ATG	CAA	CCA	GTG	558
S	D	K	Y	F	T	E	F	R	V	L	G	K	G	G	F	G	E	V	C	206
TCA	GAC	AAG	TAC	TTC	ACT	GAG	TTC	AGA	GTG	CTG	GGG	AAA	GGT	GGT	TTT	GGG	GAG	GTA	TGT	618
A	V	Q	V	K	N	T	G	K	M	Y	A	C	K	K	L	D	K	K	R	226
GCC	GTC	CAG	GTG	AAA	AAC	ACT	GGG	AAG	ATG	TAT	GCC	TGT	AAG	AAA	CTG	GAC	AAG	AAG	CGG	678
L	K	K	K	G	G	E	K	M	A	L	L	E	K	E	I	L	E	K	V	246
CTG	AAG	AAG	AAA	GGT	GGC	GAG	AAG	ATG	GCT	CTC	TTG	GAA	AAG	GAA	ATC	TTG	GAG	AAG	GTC	738
S	S	P	F	I	V	S	L	A	Y	A	F	E	S	K	T	H	L	C	L	266
AGC	AGC	CCT	TTC	ATT	GTC	TCT	CTG	GCC	TAT	GCC	TTT	GAG	AGC	AAG	ACC	CAT	CTC	TGC	CTT	798
V	M	S	L	M	N	G	G	D	L	K	F	H	I	Y	N	V	G	T	R	286
GTC	ATG	AGC	CTG	ATG	AAT	GGG	GGA	GAC	CTC	AAG	TTC	CAC	ATC	TAC	AAC	GTG	GGC	ACG	CGT	858

Fig. 1B

G	L	D	M	S	R	V	I	F	Y	S	A	Q	I	A	C	G	M	L	H	306
GGC	CTG	GAC	ATG	AGC	CGG	GTG	ATC	TTT	TAC	TCG	GCC	CAG	ATA	GCC	TGT	GGG	ATG	CTG	CAC	918
L	H	E	L	G	I	V	Y	R	D	M	K	P	E	N	V	L	L	D	D	326
CTC	CAT	GAA	CTC	GGC	ATC	GTC	TAT	CGG	GAC	ATG	AAG	CCT	GAG	AAT	GTG	CTT	CTG	GAT	GAC	978
L	G	N	C	R	L	S	D	L	G	L	A	V	E	M	K	G	G	K	P	346
CTC	GGC	AAC	TGC	AGG	TTA	TCT	GAC	CTG	GGG	CTG	GCC	GTG	GAG	ATG	AAG	GGT	GGC	AAG	CCC	1038
I	T	Q	R	A	G	T	N	G	Y	M	A	P	E	I	L	M	E	K	V	366
ATC	ACC	CAG	AGG	GCT	GGA	ACC	AAT	GGT	TAC	ATG	GCT	CCT	GAG	ATC	CTA	ATG	GAA	AAG	GTA	1098
S	Y	S	Y	P	V	D	W	F	A	M	G	C	S	I	Y	E	M	V	A	386
AGT	TAT	TCC	TAT	CCT	GTG	GAC	TGG	TTT	GCC	ATG	GGA	TGC	AGC	ATT	TAT	GAA	ATG	GTT	GCT	1158
G	R	T	P	F	K	D	Y	K	E	K	V	S	K	E	D	L	K	Q	R	406
GGA	CGA	ACA	CCA	TTC	AAA	GAT	TAC	AAG	GAA	AAG	GTC	AGT	AAA	GAG	GAT	CTG	AAG	CAA	AGA	1218
T	L	Q	D	E	V	K	F	Q	H	D	N	F	T	E	E	A	K	D	I	426
ACT	CTG	CAA	GAC	GAG	GTC	AAA	TTC	CAG	CAT	GAT	AAC	TTC	ACA	GAG	GAA	GCA	AAA	GAT	ATT	1278
C	R	L	F	L	A	K	K	P	E	Q	R	L	G	S	R	E	K	S	D	446
TGC	AGG	CTC	TTC	TTG	GCT	AAG	AAA	CCA	GAG	CAA	CGC	TTA	GGA	AGC	AGA	GAA	AAG	TCT	GAT	1338

Fig. 1C

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D	P	R	K	H	H	F	F	K	T	I	N	F	P	R	L	E	A	G	L	466	
GAT	CCC	AGG	AAA	CAT	CAT	TTC	TTT	AAA	ACG	ATC	AAC	TTT	CCT	CGC	CTG	GAA	GCT	GGC	CTA	1398	
I	E	P	P	F	V	P	P	D	P	S	V	V	Y	A	K	D	I	A	E	I	486
ATT	GAA	CCC	CCA	TTT	GTG	CCA	GAC	CCT	TCA	GTG	GTT	TAT	GCC	AAA	GAC	ATC	GCT	GAA	ATT	1458	
D	D	F	S	E	V	R	G	V	E	F	D	D	K	D	K	Q	F	F	K	506	
GAT	GAT	TTC	TCT	GAG	GTT	CGG	GGG	GTG	GAA	TTT	GAT	GAC	AAA	GAT	AAG	CAG	TTC	TTC	AAA	1518	
N	F	A	T	G	A	V	P	I	A	W	Q	E	E	I	I	E	T	G	L	526	
AAC	TTT	GCG	ACA	GGT	GCT	GTT	CCT	ATA	GCA	TGG	CAG	GAA	GAA	ATT	ATA	GAA	ACG	GGA	CTG	1578	
F	E	E	L	N	D	P	P	N	R	P	T	G	C	E	E	G	N	S	K	546	
TTT	GAG	GAA	CTG	AAT	GAC	CCC	AAC	AGA	CCT	ACG	GGT	TGT	GAG	GAG	GGT	AAT	TCA	TCC	AAG	1638	
S	G	V	C	L	L	L	*													553	
TCT	GGC	GTG	TGT	TTG	TTA	TTG	TAA													1662	

ATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAATCTGTGGA
 ATGAGGGCTAATCAGTTAGGAGGGACATCACACACCAAAACAATTCAAAGACAGGCAAGCTCACTACTAGAACACAT
 TTTATTTTCTTTTCTTCTTTCATAAAGATGAGTAAAGTCTCAGTTTTCACCTGAGGGCAGGAAAAGGAACACTCAGGT
 TTATTTTGA

Fig. 1D

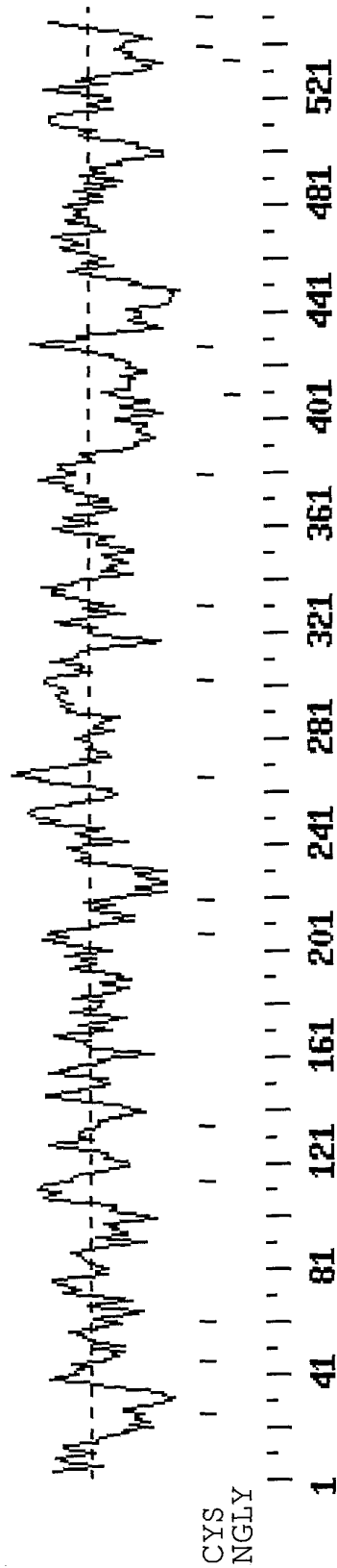


Fig. 2

FIG. 3A

69087	<u>MVDMGALDNL</u> <u>LIANTA</u>	<u>YLQARKPSDCD</u> <u>SKEL</u>	<u>QRRRRSLALPGLQGC</u>	<u>AELRQKLSLNFHSLC</u>
SGK064	MVDMGALDNL LIANTA	YLQARKPSDCD SKEL	QRRRRSLALPGLQGC	AELRQKLSLNFHSLC
ST GRK7	M-DMGGLDNL LIANTA	YLQAR-KTDS DSREL	QRRRRSLALPGQGC	AELRQSLSPHFHSLC
OL GRK7	MCDMGGLDNL LVANTA	YLKAQ---GGDDKEM	KKRRRSLSLPKPEQC	AALRSTLDKDFESLC
CC GRK7	MCDMGGLDNL LVANTA	YLKAQ---GGDDKEM	KKRRRSLSLPKPEQC	VALRESIEKDFTLIC
69087	<u>EQQPIGRRLFR</u> <u>DFLA</u>	T-VPTFRKAA <u>TFL</u> <u>ED</u>	<u>VQNWELAE</u> <u>EGPTKDS</u>	<u>ALQGLVATC</u> <u>SAPAP</u>
SGK064	EQQPIGRRLFR DFLA	T-VPTFRKAA <u>TFL</u> <u>ED</u>	VQNWELAE <u>EGPTKDS</u>	ALQGLVATC <u>SAPAP</u>
ST GRK7	EQQPIGRRLFR DFLA	T-VPKYSQAV <u>AFL</u> <u>ED</u>	VQNWELAE <u>EGPAKTS</u>	TLQQLAATC <u>ARDPGP</u>
OL GRK7	EKQPIGRFR <u>QYLD</u>	QGGPECNAA <u>AEFLDD</u>	LNDWELSEAA <u>AKDKA</u>	RTNIINK <u>FCCKDGSKS</u>
CC GRK7	ERQPIGRRLFR DFLA	N-TPEFKLA <u>AEFLDE</u>	LYDWDLA <u>EAGAAKDKA</u>	RQNIINK <u>YCKPDSKT</u>
69087	<u>GNPQPF</u> <u>LSQAVATKC</u>	<u>QAA</u> <u>TTEEE</u> <u>ERVA</u> <u>AVTL</u>	<u>RKAEAMA</u> <u>FLQE</u> <u>QPFK</u>	<u>DFVTS</u> <u>AFYDK</u> <u>FLOWK</u>
SGK064	GNPQPF <u>LSQAVATKC</u>	QAA <u>TTEEE</u> <u>ERVA</u> <u>AVTL</u>	AKAEAMA <u>FLQE</u> <u>QPFK</u>	DFVTS <u>AFYDK</u> <u>FLOWK</u>
ST GRK7	---QSF <u>LSQDLATKC</u>	RAASTDE <u>ERKTLVEQ</u>	AKAETMS <u>FLQE</u> <u>QPFQ</u>	DFLAS <u>PFYDR</u> <u>FLOWK</u>
OL GRK7	S--LT <u>FLTGDVATKC</u>	KAVTDK <u>DFEEVMG-Q</u>	VKEATKE <u>FLKGK</u> <u>PFT</u>	DYQTSE <u>FFEK</u> <u>FLOWK</u>
CC GRK7	F--LT <u>FLSGEPAEKC</u>	KSVTDAT <u>FE</u> <u>EV</u> <u>MKNK</u>	VQDGV <u>RE</u> <u>FLKGK</u> <u>PFT</u>	EYQGSQ <u>YFDK</u> <u>FLOWK</u>
69087	<u>LFEMQPVSD</u> <u>KYFTEF</u>	<u>RVLGKGG</u> <u>FGEVCAVQ</u>	<u>VKNTG</u> <u>KMYACKKLDK</u>	<u>KRLKKKG</u> <u>G</u> <u>EKMALLE</u>
SGK064	LFEMQPVSD <u>KYFTEF</u>	RVLGKGG <u>FGEVCAVQ</u>	VKNTG <u>KMYACKKLDK</u>	KRLKKKG <u>G</u> <u>EKMALLE</u>
ST GRK7	LFEMQPVSD <u>KYFTEF</u>	RVLGKGG <u>FGEVCAVQ</u>	VRNTG <u>KMYACKKLDK</u>	KRLKKKG <u>G</u> <u>EKMALLE</u>
OL GRK7	EYEKQPI <u>TEKYFYEF</u>	RTLKGKGG <u>FGEVCAVQ</u>	VKNTG <u>QMYACKKLC</u>	KRLKKKH <u>G</u> <u>EKMALLE</u>
CC GRK7	EYEKQPI <u>SDKYFYEF</u>	RTLKGKGG <u>FGEVCAVQ</u>	VKNTG <u>QMYACKKLC</u>	KRLKKKG <u>G</u> <u>EKMALLE</u>

Fig. 3A

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69087	<u>KEILEKVSSPFIVSL</u>	<u>AYAFESKTHLCLVMS</u>	<u>LMNGGDLKFHIYNVG</u>	T-----RGLDMSRV
SGK064	KEILEKVSSPFIVSL	AYAFESKTHLCLVMS	LMNGGDLKFHIYNVG	T-----RGLDMSRV
ST GRK7	KEILEKVNSPFIVSL	AYAFESKTHLCLVMS	LMNGGDLKFHIYNVG	T-----RGLAMSRV
OL GRK7	KKILEKVNSLFIVSL	AYAYDTKTHLCLVMS	LMNGGDLKYHIYNIG	-----EKGIEMERI
CC GRK7	KQILEKVNSLFLVNL	AYAYDTKTHLCLVMT	LMNGGDLKYHIYNIG	YDGKGVDKGIEMKRI
69087	<u>IFYSAQIACGMLHLH</u>	<u>ELGIVYRDMKPENVL</u>	<u>LDDLGNCRSLDLGLA</u>	<u>VEMKGGKPI</u> <u>TQ</u> <u>RAGT</u>
SGK064	IFYSAQIACGMLHLH	ELGIVYRDMKPENGL	LDDLGNCRSLDLGLA	VEMKGGKPI TQ RAGT
ST GRK7	IFYTAQMTCGVLHLH	GLGIVYRDLKPENVL	LDDLGNCRSLDLGLA	VEVQDDKPI TQ RAGT
OL GRK7	IYYTAQITTGMLQLH	NMDIVYRDMKPENVL	LDSQGQCRSLDLGLA	VEIPVGKTTTQKAGT
CC GRK7	IHYTAQITTGILHLH	DMDI IYRDMKPENVL	LDSQGQCRSLDLGLA	IEIAPGKTVTQMAGT
69087	<u>NGYMAPEILMEKVS</u> <u>Y</u>	<u>SY PVDWFAMGCSIYE</u>	<u>MVAGRTPFKD</u> ---YK	<u>EKVS</u> <u>KEDL</u> <u>KQ</u> <u>RT</u> <u>LQD</u>
SGK064	NGYMAPEILMEKVS	SY PVDWFAMGCSIYE	MVAGRTPFKD---YK	EKVS KEDL KQ RT LQD
ST GRK7	NGYMAPEILMDKASY	SY PVDWFAMGCSIYE	MVAGRTPFKD---FK	EKVS KEDL KERT MKD
OL GRK7	GAYMAPEILTETP-Y	RTSVDWWALGCSIYE	MVAGYTPFKGPEAKK	EKVEKEEVQRR IINE
CC GRK7	GAYMAPEILSKTP-Y	RTSVDWWALGCSIYE	MVAGYTPFKGPESKK	EKVEKEEVQRR ILNE
69087	<u>EVKFQHDNFT</u> <u>EEAKD</u>	<u>ICRFLAKKPEQRLG</u>	<u>SREKSDDP</u> <u>PRKH</u> <u>FFK</u>	<u>TINF</u> <u>PR</u> <u>LEAG</u> <u>LIEPP</u>
SGK064	EVKFQHDNFT EEAKD	ICRFLAKKPEQRLR	SREKSDDP PRKH FFK	TINF PR LEAG LIEPP
ST GRK7	EVAFHNFTEETKD	ICRFLAKKPEQRLG	SREKADDP PRKH FFFQ	TVNFPRL EAGLVEPP
OL GRK7	EPKFEHKNFNAPTID	IIKQFLKKKIDERLG	CKG--DDPRKH EWFK	SINFARLEAGLIDPP
CC GRK7	EPKWEHKCFDAPTKD	VIQQFLKKKIDERLG	MRNNMEDPRKH EWFK	SINFPRLEAGLVDPP

Fig. 3B

Footnote 3024400F

69087	<u>FVPDP</u> <u>SVVYAKDIAE</u>	<u>IDDFSEVRGV</u> <u>VEFDDK</u>	<u>DKQFFK</u> <u>NFATGAVPI</u>	<u>AWQEEI</u> <u>IETGLFEEEL</u>
SGK064	FVPDP <u>SVVYAKDIAE</u>	IDDFSEVRGVVEFDDK	DKQFFKNFATGAVPI	AWQEEI IETGLFEEEL
ST GRK7	FVPDP <u>SVVYAKDVDE</u>	IDDFSEVRGVVEFDDK	DKQFFQRSTGAVPV	AWQEEI IETGLFEEEL
OL GRK7	WVRKPNVYAKDTGD	IAEFSEIKGIEFDAK	DEKFFKEFFSTGAVSI	AWQEMIDTGLFDEL
CC GRK7	WVPKPNVYAKDTGD	IAEFSEIKGIEFDAK	DDKFFKEFFSTGAVPI	QWQQEM IETGLFDEL

69087	<u>NDPNR</u> <u>PTGC</u> <u>EEGNSS</u>	<u>K-SG</u> <u>VCLLL</u>
SGK064	NDPNRPTGC <u>EEGNSS</u>	K-SGVCLLL
ST GRK7	NDPNRPSGDGKGDSS	K-SGVCLLL
OL GRK7	NDPNRKESSGGLDDD	KKSGTCTLL
CC GRK7	NDPNRKEGAGGGDDE	KKSGTCALL

Fig. 3C

GGGGGAAGAGGGCTGAACCCGTCGCTGCCGGGGGTGGAGCCCCACGGCAGGCGCTGCGCCGGGTGGAGA
 CTCGGCTTCCCTCAGCCCCCTGGGGCAGAACTTCTCGCCCCCTCTCCCTCCCGCAGTGGACTCCCTCCCCAG
 CCGGCCAGTCCCTCCCGGAGAGAGCGCGCGGAGACAGCCCCGGGGGCTACCTTCCCCAGGCGAGCATC

M S A A Q V S S S R R Q S C Y L C D L P 20
 ATG TCG GCG GCG CAG GTG TCC TCG TCC CGG AGA CAA TCT TGC TAC CTG TGC GAC CTG CCC 60

R M P W A M I W D F S E P V C R G C V N 40
 CGC ATG CCC TGG GCC ATG ATC TGG GAC TTC TCG GAA CCC GTA TGC CGC GGT TGC GTC AAC 120

Y E G A D R I E F V I E T A R Q L K R A 60
 TAC GAG GGC GCT GAT CGC ATC GAA TTC GTG ATC GAG ACA GCG CGC CAG CTG AAG CGG GCG 180

H G C F P E G R S P P G A A S A A K 80
 CAC GGC TGC TTC CCG GAG GGT CGC TCC CCA CCC GGC GCG TCG GCC GCG GCG AAG 240

P P P L S A K D I L L Q Q Q Q L G H G 100
 CCG CCG CCG CTC TCC GCC AAG GAC ATC CTT TTG CAG CAG CAG CAG CTT GCG CAC GCG 300

G P E A A P R A P Q A L E R Y P L A A 120
 GGC CCC GAG GCG GCC CCG CGC GCG CAG GCC TTG GAG CGC TAC CCG TTG GCG GCC GCG 360

A E R P P R L G S D F G S S R P A A S L 140
 GCC GAG AGG CCC CCG CGC CTC GGC TCT GAC TTC GGC AGC AGC CGC CCG GCA GCG AGC CTG 420

Fig. 4A

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A	Q	P	P	T	P	P	Q	P	P	P	V	N	G	I	L	V	P	N	G	F	160
GCC	CAG	CCG	CCG	ACG	CCG	CCG	CAG	CCG	CCG	CCC	GTG	AAC	GGC	ATC	CTG	GTG	CCC	AAC	GGC	TTC	480
S	K	L	E	E	P	E	L	N	N	AAT	CGC	CAG	AGC	CCG	AAC	CCG	CGG	CGC	GGC	CAC	180
TCC	AAG	CTA	GAG	GAG	CCG	CCG	CCC	GAG	CTG	ATG	CGC	CAG	AGC	CCG	AAC	CCG	CGG	CGC	GGC	CAC	540
A	V	P	P	T	L	V	L	V	P	ATG	AAC	GGC	TCG	GCC	ACG	CCG	GCG	GCC	GCC	AGC	200
GCG	GTG	CCG	CCC	ACC	CTG	GTG	CCG	CTC	ATG	ATG	AAC	GGC	TCG	GCC	ACG	CCG	GCG	GCC	GCC	AGC	600
L	G	S	A	Q	P	T	D	L	G	G	A	H	K	R	P	A	S	V	S	S	220
CTG	GGC	TCC	GCG	CAG	CCC	ACC	ACC	GAT	CTG	GGC	GCC	CAC	AAG	CGG	CCG	GCA	TCC	GTG	TCG	AGC	660
S	A	A	V	E	H	E	Q	R	E	A	A	A	A	K	E	K	Q	P	P	P	240
AGC	GCT	GCC	GTG	GAG	CAC	GAG	CAG	CGT	GAG	GCG	GCA	GCC	AAG	GAG	GAG	AAA	CAA	CCG	CCG	CCG	720
P	A	H	R	G	P	A	D	S	L	S	T	A	A	A	G	A	A	E	L	S	260
CCT	GCG	CAC	CGG	GGC	CCG	CCG	GAC	AGC	CTG	TCC	ACC	GCG	GCC	GCC	GGG	GCC	GCC	GAG	CTG	AGC	780
A	E	G	A	G	K	S	R	G	S	G	E	Q	D	W	V	N	R	P	K	K	280
GCG	GAA	GGT	GCG	GGC	AAG	AGC	CGC	GGG	TCT	GGA	GAG	CAG	GAC	TGG	GTC	AAC	AGG	CCC	AAG	AAG	840
T	V	R	D	T	L	L	A	L	H	Q	H	G	H	S	G	P	F	E	S	S	300
ACC	GTG	CGC	GAC	ACG	CTG	CTG	GCG	CTG	CAC	CAG	CAC	GGC	CAC	TCG	GGG	CCC	TTC	GAG	AGC	AGC	900

Fig. 4B

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K F K K K E P A L T A G R L L G F E A N G 320
AAG TTT AAG AAG GAG CCG GCC CTG ACT GCA GGC AGG TTG TTG GGT TTC GAG GCC AAC GGG 960

A N G S K A V A R T A R K R K P S P E P 340
GCC AAC GGG TCT AAA GCA GTT GCA AGA ACA GCA AGG AAA AGG AAG CCC TCT CCA GAA CCA 1020

E G E V G P P K I N G E A Q P W L S T S 360
GAA GGT GAA GTC GGG CCC CCT AAG ATC AAC GGA GAG GCC CAG CCG TGG CTG TCC ACA TCC 1080

T E G L K I P M T P T S S F V S P P P P 380
ACA GAG GGG CTC AAG ATC CCC ATG ACT CCT ACA TCC TCT TTT GTG TCT CCG CCA CCA CCC 1140

T A S P H S N R T T P P E A A Q N G Q S 400
ACT GCC TCA CCT CAT TCC AAC CGG ACC ACA CCG CCT GAA GCG GCC CAG AAT GGC CAG TCC 1200

P M A A A L I L V A D N A G G S H A S K D 420
CCC ATG GCA GCC CTG ATC TTA GTA GCA GAC AAT GCA GGG GGC AGT CAT GCC TCA AAA GAT 1260

A N Q V H S T T R R R N S N S P S P S 440
GCC AAC CAG GTT CAC TCC ACT ACC AGG AGG AAT AGC AAC AGT CCG CCC TCT CCG TCC TCT 1320

M N Q R R L G P R R E V G G G G G CAG GGA GCA GGC AAC ACA GGA 460
ATG AAC CAA AGA AGG CTG GGC CCC AGA GAG GTG GGG GGC CAG GGA GCA GGC AAC ACA GGA 1380

Fig. 4C

[illegible]

CTTTTCCGGTTTCAGAAAAAACCCTTAATTAATAACTGCTTGAATTGTATATATATATCTCCATATATATAT
ATATCAAGACAAAGGAAATGTAGACTTCATAAACATGCTGTATAAATTTTGATTTTGTGAATACATTTGTTTCTA
TATTTTTCACGACAAAAAGGTATGTACTTATAAGACATTTTTTCTTTTGTAACTTATAGCATATCTTTGTGC
TTTATTATCCTGGTGACAGTTACCGTTCTATGTAGGCTGTGACTTGCCTGCTTTTATAGACACTTGGCAAAATCAGAA
ATGCTTCTAGCTGTATTGTATGCACCTATTTAAAAAGAAAAAAGCCAAATACATTTTCTGAACCTTTGTAAAGAT
TGCCCTTACTGCTGTCAATTCCTTATTGCTGGCCCCCTTCTCAGGCCGAGGCCAAGTGTGGAGAGGAAAGGAAATGA

Fig. 4D

Fig. 4E

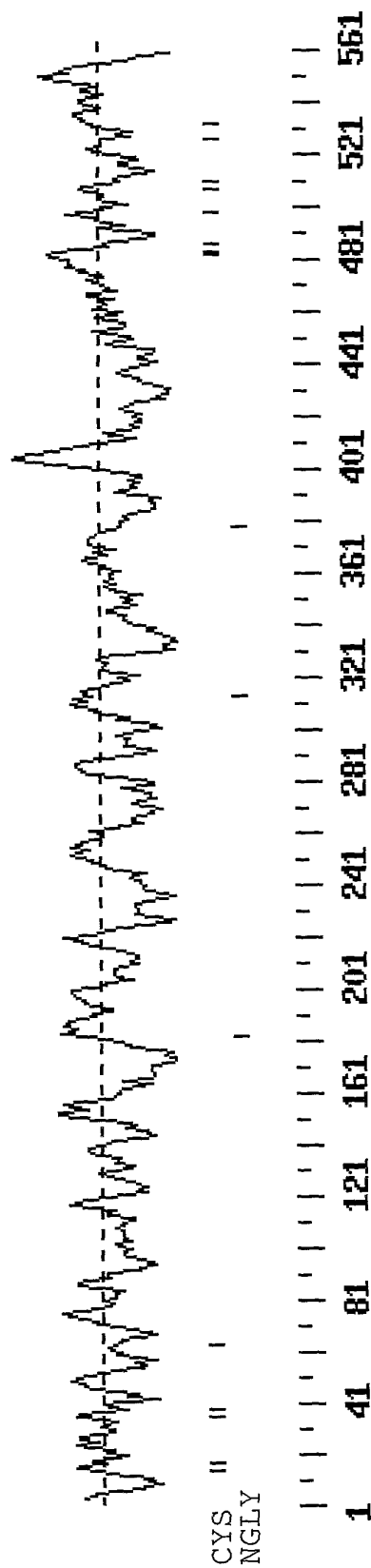


Fig. 5

FIG 6A

15821	MSAAQVSSRRQSCY	LCDLPRMPWMIWDF	SEPVCRGCVNYEGAD	RIEFVIETARQLKRA
C14orf4	MSAAQVSSRRQSCY	LCDLPRMPWMIWDF	SEPVCRGCVNYEGAD	RIEFVIETARQLKRA
KIAA1865	-----	-----	-----	-----
15821	HG-----	CFPEGRSPPGAAASA	AAKPPPLSAKDILLQ	QQQQLGHGGPEAAPR
C14orf4	HGCFQDGRSPGPPPP	VGVKTVALSAKEAAA	AAAAAAAAAAAAQQQ	QQQQQQQQQQQQQQ
KIAA1865	-----SH	RIRDRDSAPAEAGAR	LLPGRPLPRAAAAAQ	QQQQQQQQQQQQQQ
15821	APQALERYPLAAAAE	RPPRLGSDFGSSRP-	-----AAS	LAQPPTPQPPP----
C14orf4	QQQQQQQLNHVDGSS	KPAVLAAPSGLERYG	LSAAAAAAAAAAAAAV	EQRSRFEYPPPPVSL
KIAA1865	QQQQQQQLNHVDGSS	KPAVLAAPSGLERYG	LSAAAAAAAAAAAAAV	EQRSRFEYPPPPVSL
15821	-----VNGILV	PNGFSK---LEEPPE	LNRQSPNP-----	-----
C14orf4	GSSSHTARLPNGLGG	PNGFPKPTPEEGPPE	LNRQSPNSSSAAASV	ASRRGTHGGLVTGLP
KIAA1865	GSSSHTARLPNGLGG	PNGFPKPTPEEGPPE	LNRQSPNSSSAAASV	ASRRGTHGGLVTGLP
15821	---RRG---HAVPPT	LVPLMNGSATPAAAS	LGSAQPTDLG-----	-----AHKRP--AS
C14orf4	NPGGGGGPQLTVPPN	LLPQTLNLNGPASAAV	LPPPPPHALGSRGPP	TPAPPGAPGGPACLG
KIAA1865	NPGGGGGPQLTVPPN	LLPQTLNLNGPASAAV	LPPPPPHALGSRGPP	TPAPPGAPGGPACLG

FIG 6A

FIG. 6B

15821	-----VSSS	AAVEHEQREAAAKEK	QPPPPAHRGPADSL	TAAGAAELSAEGAGK
C14orf4	GTPGVSATSSSASS	TSSSVAEVGVGAGGK	RPGSVSTDQERELK	EKQRNAEALAEELSES
KIAA1865	GTPGVSATSSSASS	TSSSVAEVGVGAGGK	RPGSVSTDQERELK	EKQRNAEALAEELSES
15821	SRGSGEQDWVNRPKT	VRDTLLALH-----	-----	-----
C14orf4	LRN-RAEEWASKPKM	VRDTLLTLTAGCTPYE	VRFKKDHSLLG RVFA	FDAVSKPGMDYELKL
KIAA1865	LRN-RAEEWASKPKM	VRDTLLTLTAGCTPYE	VRFKKDHSLLG RVFA	FDAVSKPGMDYELKL
15821	-----	-----	-----	-----QHGHS GP
C14orf4	FIEYPTGSGNVYSSA	SGVAKQMYQDCMKDF	GRGLSSGFKYLEYEK	KHGS GDWRLLG DLLP
KIAA1865	FIEYPTGSGNVYSSA	SGVAKQMYQDCMKDF	GRGLSSGFKYLEYEK	KHGS GDWRLLG DLLP
15821	FESKFKE-----	-----P-----	-----ALTAGRLL	GFEANGANGSKAVAR
C14orf4	EAVRFFKEGVPGADM	LPQPYLDASCPMLPT	ALVSLSRAPSAPP GT	GALPPAAPSGRGAAA
KIAA1865	EAVRFFKEGVPGADM	LPQPYLDASCPMLPT	ALVSLSRAPSAPP GT	GALPPAAPSGRGAAA
15821	TARKRKPSPEPEGEV	GPPKINGEAQP---W	LSTSTEGLKIPMTPT	SSFVS-----PP
C14orf4	SLRKRKASPEPPDSA	EGALKLGEEQQRQW	MANQSEALKLTMSAG	GFAAPGHAAGGPPPP
KIAA1865	SLRKRKASPEPPDSA	EGALKLGEEQQRQW	MANQSEALKLTMSAG	GFAAPGHAAGGPPPP

FIG. 6B

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15821	PPTASPHSNRRTTPPE	AAQ-NGQSPMAALIL	VADNAGGSHASKDAN	QVHSTTR--R-NSNS
C14orf4	PPPLGPHSNRRTTPPE	SAPQNGPSPMAALMS	VADTLGTAHSPKDG	SVHSTTASARRNSSS
KIAA1865	PPPLGPHSNRRTTPPE	SAPQNGPSPMAALMS	VADTLGTAHSPKDG	SVHSTTASARRNSSS
15821	PPSPSSMN-QRRRLGP	R-----EVGGQGAG	NTGGLEPVHPASLPD	SSLATSAPLCCTICH
C14orf4	PVSPASVPGQRRRLAS	RNGDLNLQVAPPPPS	AHPGMDQVHPQNIPD	SPMANSGPLCCTICH
KIAA1865	PVSPASVPGQRRRLAS	RNGDLNLQVAPPPPS	AHPGMDQVHPQNIPD	SPMANSGPLCCTICH
15821	ERLEDTHFVQCPSVP	SHKFCFPSCRQSIKQ	QGASGEVYCPSGEKC	PLVGSNVPWAFMQGE
C14orf4	ERLEDTHFVQCPSVP	SHKFCFPSCRRESIKA	QGATGEVYCPSGEKC	PLVGSNVPWAFMQGE
KIAA1865	ERLEDTHFVQCPSVP	SHKFCFPSCRRESIKA	QGATGEVYCPSGEKC	PLVGSNVPWAFMQGE
15821	IATILAGDVKKKER	DS		
C14orf4	IATILAGDVKKKER	DP		
KIAA1865	IATILAGDVKKKER	DP		

FIG. 6C

FIG. 6C

T0220T"5024400T

15821	GFEANGANGKAVAR	TARKRKPSPEPEGEV	GPPKINGEAQ---W	LSTSTEGLKIPMTPT
C14orf4	GALPPAAPSGRGAAA	SLRKRKASPEPPDSA	EGALKLGEEQQRQW	MANQSEALKLTMSAG
KIAA1865	GALPPAAPSGRGAAA	SLRKRKASPEPPDSA	EGALKLGEEQQRQW	MANQSEALKLTMSAG
736	-----VAR	TARKRKPSPEPEGEV	GPPKINGEAQ---W	XSTSTEGXKIPMTPT
HTRM	-----	-----	-----	-----MTPT
dn740_3	-----	-----	-----	-----MTPT
Unnamed	-----	-----	-----	-----MSAG
15821	SSFVS-----PP	PPTASPHSNRTTPPE	AAQ-NGQSPMAALIL	VADNAGGSHASKDAN
C14orf4	GFAAPGHAAGGPPPP	PPPLGPHSNRTTPPE	SAPQNGPSPMAALMS	VADTLGTAHSPKDG
KIAA1865	GFAAPGHAAGGPPPP	PPPLGPHSNRTTPPE	SAPQNGPSPMAALMS	VADTLGTAHSPKDG
736	SSFVS-----PP	PPTASPHSNRTTPPE	AAQ-NGQSPMAALIL	VADNAGGSHASKDAN
HTRM	SSFVS-----PP	PPTASPHSNRTTPPE	AAQ-NGQSPMAALIL	VADNAGGSHASKDAN
dn740_3	SSFVS-----PP	PPTASPHSNRTTPPE	AAQ-NGQSPMAALIL	VADNAGGSHASKDAN
Unnamed	GFAAPGHAAGGPPPP	PPPLGPHSNRTTPPE	SAPQNGPSPMAALMS	VADTLGTAHSPKDG
15821	QVHSTTR--R-NSNS	PPSPSSMN-QRRLLGP	R-----EVGGQGAG	NTGGLEPVHPASLPD
C14orf4	SVHSTTASARRNSS	PVSPASVPGQRRLLAS	RNGDLNLQVAPPPPS	AHPGMDQVHPQNI
KIAA1865	SVHSTTASARRNSS	PVSPASVPGQRRLLAS	RNGDLNLQVAPPPPS	AHPGMDQVHPQNI
736	QVHSTTRR---NSNS	PPSPSSMN-QRRLLGP	R-----EVGGQGAG	NTGGLEPVHPASLPD
HTRM	QVHSTTRR---NSNS	PPSPSSMN-QRRLLGP	R-----EVGGQGAG	NTGGLEPVHPASLPD
dn740_3	QVHSTTRR---NSNS	PPSPSSMN-QRRLLGP	R-----EVGGQGAG	NTGGLEPVHPASLPD
Unnamed	SVHSTTASARRNSS	PVSPASVPGQRRLLAS	RNGDLNLQVAPPPPS	AHPGMDQVHPQNI

FIG. 7A

FIG. 7B

15821	SSLATSAPLCCTLCH	ERLEDTHFVQCPSVP	SHKFCFP C SRQSIQ	QGASGEVY C PSGEKC
C14orf4	SPMANSGPLCCTICH	ERLEDTHFVQCPSVP	SHKFCFP C SRRESIKA	QGATGEVY C PSGEKC
KIAA1865	SPMANSGPLCCTICH	ERLEDTHFVQCPSVP	SHKFCFP C SRRESIKA	QGATGEVY C PSGEKC
736	FSLATSAPLCCTLCH	ERLEDNHFVQC---	-----	-----
HTRM	SSLATSAPLCCTLCH	ERLEDTHFVQCPSVP	SHKFCFP C SRQSIQ	QGASGEVY C PSGEKC
dn740_3	SSLATSAPLCCTLCH	ERLEDTHFVQCPSVP	SHKFCFP C SRQSIQ	QGASGEVY C PSGEKC
Unnamed	SPMANSGPLCCTICH	ERLEDTHFVQCPSVP	SHKFCFP C SRRESIKA	QGATGEVY C PSGEKC
15821	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DS	
C14orf4	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DP	
KIAA1865	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DP	
736	-----	-----	--	
HTRM	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DS	
dn740_3	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DS	
Unnamed	PLVGSNVVPWAFMQGE	IATILAGDVKVKKER	DP	

FIG. 7B

Footnote 5024400F

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GTCGACCACGCGTCCGGGAGACAGAAAGAGGGTGGTGCCGATAGCTGGTCTCTTTCTCCAACACCTAGCCTGAGACT																		18
TGGCGCGCGGCTGCTATCCTGAACCTAGCTTGGTAAGTGTGTCCCGAACCCAGCGTAGAGACCTCGGACCAGCCG																		54
M T A S A S S F S S S Q G V Q Q P S																		18
CCTTG ATG ACA GCA TCC GCG TCC TCC TCC TCA TCA TCT CAG GGT GTC CAG CAG CCC TCC																		54
I Y S F S Q I T R S L F L S N G V A A N																		38
ATC TAC AGC TTC TCC CAA ATA ACC AGA AGC TTG TTT CTC AGC AAT GGT GTG GCC GCC AAC																		114
D K L L L S S N R I T A I V N A S V E V																		58
GAC AAA CTC CTT CTG TCC AGC AAT CGC ATC ACC GCC ATT GTC AAT GCC TCG GTG GAA GTG																		174
V N V F F E G I Q Y I K V P V T D A R D																		78
GTC AAC GTA TTC TCC GAG GGC ATT CAG TAC ATA AAG GTG CCT GTT ACC GAT GCT CGT GAC																		234
S R L Y D F F I A D L I H T I D M R																		98
TCG CGT CTC TAC GAC TTT TTT GAC CCC ATT GCT GAT CTT ATC CAC ACC ATC GAT ATG AGG																		294
Q G R T L L H C M A G V S R S A S L C L																		118
CAG GGC CGT ACG CTG CTG CAC TGC ATG GCT GGA GTG AGC CGT TCC GCC TCA CTG TGC CTT																		354
A Y L M K Y H S M S L L D A H T W T K S																		138
GCG TAC CTC ATG AAA TAC CAC TCC ATG TCG CTG CTG GAC GCC CAT ACA TGG ACC AAG TCG																		414

Fig. 8A

R	R	P	I	I	R	P	N	N	G	F	W	E	Q	L	I	N	Y	E	F	158
CGC	CGC	CCC	ATC	ATC	CGG	CCC	AAC	AAC	GGC	TTT	TGG	GAA	CAG	CTC	ATC	AAT	TAC	GAA	TTC	474
K	L	F	N	N	N	T	V	R	M	I	N	S	P	V	G	N	I	P	D	178
AAG	CTG	TTT	AAT	AAC	AAC	ACC	GTG	CGC	ATG	ATC	AAC	TCG	CCG	GTA	GGT	AAC	ATC	CCT	GAC	534
I	Y	E	K	D	L	R	T	M	I	S	M	*								190
ATC	TAT	GAG	AAG	GAC	CTA	CGT	ACG	ATG	ATA	TCA	ATG	TAA								573
GCCATCCCGCCAGCCCTGACATCTGCCATCGATCTGCACCAAGACTGAACCTGAACACTGACATTTTGTAGTAAA																				
GAAAACCGGATGGTGCCTTGTAAAGGGCAAGAAAAAAGGAGGGGTTGGAGTTTGAACGTAAGTAAAGCCTTACCTTA																				
ATAGAATTAAATTCATGAACACATAAAACA																				

Fig. 8B

TECHNICAL SUPPORT

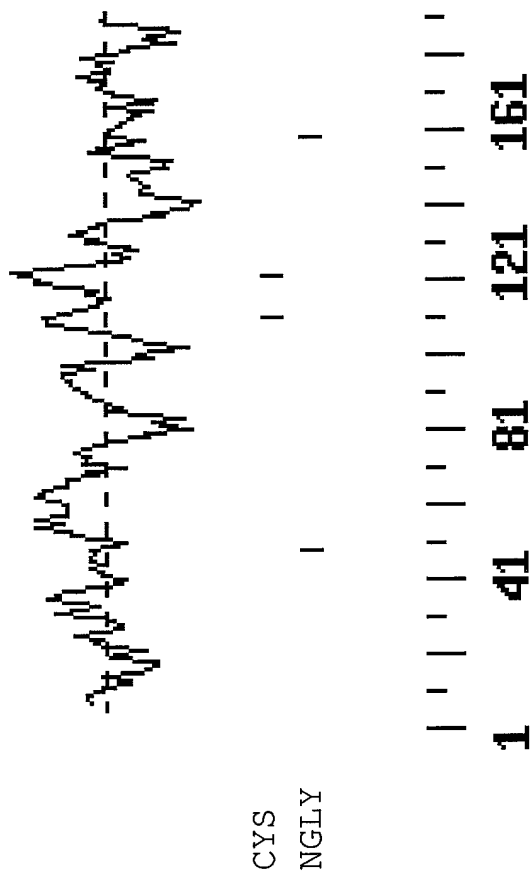


Fig. 9

"SECRET" SEQUENCE

15814 1 MTASASSFSSQGVQQPSIYSFSQITRSLFLSNGVAANDKLLSSNRITAIVNASVEVN 60
|||||
DSP-8 1 MTASASSFSSQGVQQPSIYSFSQITRSLFLSNGVAANDKLLSSNRITAIVNASVEVN 60
|||||

15814 61 VFFEGIQYIKVPVTDARDSRLYDFFDPIADLIHTIDMRQGRLLHCMAGVSRASLCLAY 120
|||||
DSP-8 61 VFFEGIQYIKVPVTDARDSRLYDFFDPIADLIHTIDMRQGRLLHCMAGVSRASLCLAY 120
|||||

15814 121 LMKYHSMALLDAHTWTKSRRIIRPNNGFWEQLINYEFKLFNNNTVRMINSPVGNIPDIY 180
|||||
DSP-8 121 LMKYHSMALLDAHTWTKSRRIIRPNNGFWEQLINYEFKLFNNNTVRMINSPVGNIPDIY 180
|||||

15814 181 EKDLRTMISM 190
|||||
DSP-8 181 EKDLRMMISM 190
|||||

Fig. 10